

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/577,781
Source: IFWP
Date Processed by STIC: 6/5/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/05/2006

PATENT APPLICATION: US/10/577,781

TIME: 10:03:24

Input Set : A:\Sequence Listing 4439-4042.txt

Output Set: N:\CRF4\06052006\J577781.raw

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3 <110> APPLICANT: Masayoshi Yamaguchi
5 <120> TITLE OF INVENTION: Hyperlipidemia/Hyperalbuminemia Model Animal
7 <130> FILE REFERENCE: 4439-4042
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/577,781
C--> 9 <141> CURRENT FILING DATE: 2006-04-28
9 <150> PRIOR APPLICATION NUMBER: JP2003-374098
10 <151> PRIOR FILING DATE: 2003-11-04
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 900
18 <212> TYPE: DNA
19 <213> ORGANISM: Rattus norvegicus
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(900)
25 <400> SEQUENCE: 1
26 atg tct tcc atc aag att gaa tgt gtt tta agg gag aac tac agg tgt 48
27 Met Ser Ser Ile Lys Ile Glu Cys Val Leu Arg Glu Asn Tyr Arg Cys
28 1 5 10 15
30 ggg gag tcc cct gtg tgg gag gag gca tca aag tgt ctg ctg ttt gta 96
31 Gly Glu Ser Pro Val Trp Glu Glu Ala Ser Lys Cys Leu Leu Phe Val
32 20 25 30
34 gac atc cct tca aag act gtc tgc cga tgg gat tcg atc agc aat cga 144
35 Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
36 35 40 45
38 gtg cag cga gtt ggt gta gat gcc cca gtc agt tca gtg gca ctt cga 192
39 Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
40 50 55 60
42 cag tca gga ggc tat gtt gcc acc att gga acc aag ttc tgt gct ttg 240
43 Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
44 65 70 75 80
46 aac tgg gaa gat caa tca gta ttt atc cta gcc atg gtg gat gaa gat 288
47 Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
48 85 90 95
50 aag aaa aac aat cga ttc aat gat ggg aag gtg gat cct gct ggg aga 336
51 Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
52 100 105 110
54 tac ttt gct ggt acc atg gct gag gaa acc gcc cca gct gtt ctg gag 384
55 Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
56 115 120 125
58 cgg cac caa ggg tcc ttg tac tcc ctt ttt cct gat cac agt gtg aag 432
59 Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys

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60      130      135      140
62 aaa tac ttt aac caa gtg gat atc tcc aat ggt ttg gat tgg tcc ctg 480
63 Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
64 145      150      155      160
66 gac cat aaa atc ttc tac tac att gac agc ctg tcc tac act gtg gat 528
67 Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
68      165      170      175
70 gcc ttt gac tat gac ctg cca aca gga cag att tcc aac cgc agg act 576
71 Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
72      180      185      190
74 gtt tac aag atg gaa aaa gat gaa caa atc cca gat gga atg tgc att 624
75 Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
76      195      200      205
78 gat gtt gag ggg aag ctt tgg gtg gcc tgt tac aat gga gga aga gta 672
79 Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
80      210      215      220
82 att cgc cta gat cct gag aca ggg aaa aga ctg caa act gtg aag ttg 720
83 Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
84 225      230      235      240
86 cct gtt gat aaa aca act tca tgc tgc ttt gga ggg aag gat tac tct 768
87 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
88      245      250      255
90 gaa atg tac gtg aca tgt gcc agg gat ggg atg agc gcc gaa ggt ctt 816
91 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
92      260      265      270
94 ttg agg cag cct gat gct ggt aac att ttc aag ata aca ggt ctt ggg 864
95 Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
96      275      280      285
98 gtc aaa gga att gct cca tat tcc tat gca ggg taa 900
99 Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
100      290      295
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 299
105 <212> TYPE: PRT
106 <213> ORGANISM: Rattus norvegicus
108 <400> SEQUENCE: 2
109 Met Ser Ser Ile Lys Ile Glu Cys Val Leu Arg Glu Asn Tyr Arg Cys
110 1      5      10      15
111 Gly Glu Ser Pro Val Trp Glu Glu Ala Ser Lys Cys Leu Leu Phe Val
112      20      25      30
113 Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg
114      35      40      45
115 Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg
116      50      55      60
117 Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
118 65      70      75      80
119 Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp
120      85      90      95
121 Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg

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122          100          105          110
123 Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
124          115          120          125
125 Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys
126          130          135          140
127 Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
128 145          150          155          160
129 Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp
130          165          170          175
131 Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr
132          180          185          190
133 Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile
134          195          200          205
135 Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
136          210          215          220
137 Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
138 225          230          235          240
139 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
140          245          250          255
141 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
142          260          265          270
143 Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
144          275          280          285
145 Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
146          290          295
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 24
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer huRC-1
158 <400> SEQUENCE: 3
159 ggaggctatg ttgccaccat tgga 24
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 23
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer huRC-2
170 <400> SEQUENCE: 4
171 ccctccaaag cagcatgaag ttg 23

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date